



SEQUENCE LISTING

<110> Michael C. Chen
Chuang-Jiun Chiou
Zhongming Li
Dong-Sheng Chen

<120> COMPOSITIONS AND METHODS FOR TREATING OR
PREVENTING PNEUMOCOCCAL INFECTION

<130> 12844-002001

<140> US 10/702,305

<141> 2003-11-06

<150> US 60/424,497

<151> 2002-11-07

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 471

<212> PRT

<213> Streptococcus pneumoniae

<400> 1

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			20					25					30				
Ile	Lys	Glu	Gly	Asn	Gln	Leu	Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg		
		35					40					45					
Lys	Lys	Arg	Ser	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala		
		50				55					60						
Thr	Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val	Asp	Glu		
65					70				75					80			
Thr	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala	Val	Asp	Arg	Ala	Pro		
				85					90					95			
Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe		
			100					105					110				
Leu	Gln	Val	Glu	Asp	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn		
		115					120					125					
Asp	Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val		
		130				135					140						
Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu	Gln		
145				150						155				160			
Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu		
			165					170					175				
Asp	Ile	Asp	Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile		
			180				185					190					
Val	Asn	Phe	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys		
		195				200						205					
Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys		
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Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val
 225 230 235 240
 Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser
 245 250 255
 Asp Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val
 260 265 270
 Ala Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys
 275 280 285
 Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr
 290 295 300
 Gly Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe
 305 310 315 320
 Thr Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu
 325 330 335
 Arg Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu
 340 345 350
 Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser
 355 360 365
 Gly Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asn Glu Leu Ser Tyr
 370 375 380
 Asp His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn
 385 390 395 400
 Gly Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly
 405 410 415
 Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala
 420 425 430
 Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val
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 450 455 460
 Glu Asp Lys Val Glu Asn Asp
 465 470

<210> 2
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 <213> Artificial Sequence

<220>
 <223> primer

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38

<210> 3
 <211> 34
 <212> DNA
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<220>
 <223> primer

<400> 3
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34

<210> 4
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<212> DNA
 <213> Artificial Sequence

<220>
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<400> 4
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<210> 5
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<220>
 <223> primer

<400> 5
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<210> 6
 <211> 35
 <212> DNA
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<220>
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<400> 6
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<210> 7
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 <212> DNA
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<220>
 <223> primer

<400> 7
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<210> 8
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 8
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<210> 9
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetically generated construct

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gatgagtttg	ttgttatcga	aagaaagaag	cggagcttgt	cgacaaatac	aagtgatatt	180
tctgtaacag	ctaccaacga	cagtcgcctc	tatcctggag	cacttctcgt	agtggatgag	240
accttggttag	agaataatcc	cactcttctt	gcggtcgcgc	gtgctccgat	gacttatagt	300
attgatttgc	ctggtttggc	aagtagcgat	agctttctcc	aagtggaaga	ccccagcaat	360
tcaagtgttc	gcgagcggt	aaacgatttg	ttggctaagt	ggcatcaaga	ttatggtcag	420
gtcaataatg	tcccagctag	aatgcagtat	gaaaaaatca	cggctcacag	catggaacaa	480
ctcaaggtca	agtttggttc	tgactttgaa	aagacaggga	attctcttga	tattgatttt	540
aactctgtcc	attcaggcga	aaagcagatt	cagattgtta	attttaagca	gatttattat	600
acagtcagcg	tagatgctgt	taaaaatcca	ggagatgtgt	ttcaagatac	tgtaacggta	660
gaggatttaa	aacagagagg	aatttctgca	gagcgtcctt	tggtctatat	ttcgagtgtt	720
gcttatgggc	gccaagtcta	tctcaagttg	gaaaccacga	gtaagagtga	tgaagtagag	780
gctgcttttg	aagctttgat	aaaaggagtc	aaggtagctc	ctcagacaga	gtggaaacag	840
attttggaca	atacagaagt	gaaggcgggt	attttagggg	gcgacccaag	ttcgggtgcc	900
cgagttgtaa	caggcaaggt	ggatatggta	gaggacttga	ttcaagaagg	cagtcgcttt	960
acagcagatc	atccaggctt	gccgatttcc	tatacaactt	cttttttacg	tgacaatgta	1020
gttgcgacct	ttcaaaatag	tacagactat	gttgagacta	aggttacagc	ttacagaaac	1080
ggagatttac	tgctggatca	tagtggtgcc	tatgttgccc	aatattatat	tacttgggaat	1140
gaattatcct	atgatcatca	aggtaaggaa	gtcttgactc	ctaaggcttg	ggacagaaat	1200
gggcaggatt	taacggctca	ctttaccact	agtattcctt	taaaaggga	tggttcgtaat	1260
ctctctgtca	aaattagaga	gcgttcgggg	cttgcttggg	aatggtggcg	tacggtttat	1320
gaaaaaacgg	atttgccact	agtgcgtaag	cggacgattt	ctatttgggg	aacaactctc	1380
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<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

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gatgagtttg	ttgttatcga	aagaaagaag	cggagcttgt	cgacaaatac	aagtgatatt	180
tctgtaacag	ctaccaacga	cagtcgcctc	tatcctggag	cacttctcgt	agtggatgag	240
accttggttag	agaataatcc	cactcttctt	gcggtcgcgc	gtgctccgat	gacttatagt	300
attgatttgc	ctggtttggc	aagtagcgat	agctttctcc	aagtggaaga	ccccagcaat	360
tcaagtgttc	gcgagcggt	aaacgatttg	ttggctaagt	ggcatcaaga	ttatggtcag	420
gtcaataatg	tcccagctag	aatgcagtat	gaaaaaatca	cggctcacag	catggaacaa	480
ctcaaggtca	agtttggttc	tgactttgaa	aagacaggga	attctcttga	tattgatttt	540
aactctgtcc	attcaggcga	aaagcagatt	cagattgtta	attttaagca	gatttattat	600
acagtcagcg	tagatgctgt	taaaaatcca	ggagatgtgt	ttcaagatac	tgtaacggta	660
gaggatttaa	aacagagagg	aatttctgca	gagcgtcctt	tggtctatat	ttcgagtgtt	720
gcttatgggc	gccaagtcta	tctcaagttg	gaaaccacga	gtaagagtga	tgaagtagag	780
gctgcttttg	aagctttgat	aaaaggagtc	aaggtagctc	ctcagacaga	gtggaaacag	840
attttggaca	atacagaagt	gaaggcgggt	attttagggg	gcgacccaag	ttcgggtgcc	900
cgagttgtaa	caggcaaggt	ggatatggta	gaggacttga	ttcaagaagg	cagtcgcttt	960
acagcagatc	atccaggctt	gccgatttcc	tatacaactt	cttttttacg	tgacaatgta	1020
gttgcgacct	ttcaaaatag	tacagactat	gttgagacta	aggttacagc	ttacagaaac	1080

ggagattttac	tgctggatca	tagtgggtgcc	tatgttgccc	aatattatat	tacttggaat	1140
gaattatcct	atgatcatca	aggtaaggaa	gtcttgactc	ctaaggcttg	ggacagaaat	1200
gggcaggatt	taacggctca	ctttaccact	agtattcctt	taaaagggaa	tggtcgtaat	1260
ctctctgtca	aaattagaga	gcgttcgagg	cttgccctggg	aatgggtggcg	tacggtttat	1320
gaaaaaacgg	atttgccact	agtgcgtaag	cggacgattt	ctatttgagg	aacaactctc	1380

<210> 11

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

gactaagctt	gccaccatgg	aaattaatgt	gagtaaatta	ag	42
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<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 12

ctgactcgag	ttattttact	gtaatcaagc	catc	34
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<210> 13

<211> 954

<212> DNA

<213> Artificial Sequence

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<223> pSA-59 Aly insert

<400> 13

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tatcattggc	ggaaagaccc	agaattaggt	tttttctcgc	acattgttgg	gaacggatgc	180
atcatgcagg	taggacctgt	taataatggt	gcctgggacg	ttgggggagg	ttggaatgct	240
gagacctatg	cagcgggtga	actgattgaa	agccattcaa	ctaaagaaga	gttcatgacg	300
gactaccgcc	tttatatcga	actcttacgc	aatctagcag	atgaagcagg	tttgccgaaa	360
acgcttgata	cagggagttt	agctggaatt	aaaacgcacg	agtattgcac	gaataaccaa	420
ccaaacaacc	actcagacca	tgtggatcca	tacccttact	tggcaaatg	gggcattagc	480
cgtgagcagt	ttaagcatga	tattgagaac	ggcttgacga	ttgaaacagg	ctggcagaag	540
aatgacactg	gctactggta	cgtacattca	gacggctctt	atccaaaaga	caagtttgag	600
aaaatcaatg	gcacttggtg	ctactttgac	agttcaggct	atatgcttgc	agaccgctgg	660
aggaagcaca	cagacggcaa	ttggtactac	tttgaccaat	caggcgaaat	ggctacaggc	720
tggaagaaaa	tcgctgagaa	gtggtactat	ttcaacgaag	aaggtgccat	gaagacaggc	780
tgggtcaagt	acaaggacac	ttggtactac	ttagacgcta	aagaaggcgc	aatggtatca	840
aatgccttta	tccagtcagc	ggacggaaca	ggctggtact	acctcaaacc	agacggaaca	900
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<210> 14

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide of pSA-59 Aly insert sequence

<400> 14

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Val Gln Pro Tyr Arg Gln Val His Ala His Ser Thr Gly Asn Pro His
          20           25           30
Ser Thr Val Gln Asn Glu Ala Asp Tyr His Trp Arg Lys Asp Pro Glu
          35           40           45
Leu Gly Phe Phe Ser His Ile Val Gly Asn Gly Cys Ile Met Gln Val
          50           55           60
Gly Pro Val Asn Asn Gly Ala Trp Asp Val Gly Gly Gly Trp Asn Ala
65           70           75           80
Glu Thr Tyr Ala Ala Val Glu Leu Ile Glu Ser His Ser Thr Lys Glu
          85           90           95
Glu Phe Met Thr Asp Tyr Arg Leu Tyr Ile Glu Leu Leu Arg Asn Leu
          100          105          110
Ala Asp Glu Ala Gly Leu Pro Lys Thr Leu Asp Thr Gly Ser Leu Ala
          115          120          125
Gly Ile Lys Thr His Glu Tyr Cys Thr Asn Asn Gln Pro Asn Asn His
          130          135          140
Ser Asp His Val Asp Pro Tyr Pro Tyr Leu Ala Lys Trp Gly Ile Ser
145          150          155          160
Arg Glu Gln Phe Lys His Asp Ile Glu Asn Gly Leu Thr Ile Glu Thr
          165          170          175
Gly Trp Gln Lys Asn Asp Thr Gly Tyr Trp Tyr Val His Ser Asp Gly
          180          185          190
Ser Tyr Pro Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr
          195          200          205
Phe Asp Ser Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr
          210          215          220
Asp Gly Asn Trp Tyr Tyr Phe Asp Gln Ser Gly Glu Met Ala Thr Gly
225          230          235          240
Trp Lys Lys Ile Ala Glu Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala
          245          250          255
Met Lys Thr Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp
          260          265          270
Ala Lys Glu Gly Ala Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp
          275          280          285
Gly Thr Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Lys
          290          295          300
Pro Glu Phe Thr Val Glu Pro Asp Gly Leu Ile Thr Val Lys
305          310          315

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<210> 15

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 15

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<210> 16
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 16
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37

<210> 17
 <211> 1377
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSA-60 PspA insert

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 cagaaaaaat atgatgagga tcagaagaaa actgaggcaa aagcggataa ggaagcaaaa 180
 gcatctgcgg aaatagataa agccacgttt gctgtacaaa gtgcgtatgt aaaattttta 240
 aatgtccaat ctaatcgtca aatttcggag aatgaacgaa aaaaacaatt agcagaaata 300
 gataaagaga tagagaatgc taaacaaaat ttacagaata aacaggaaga atttaataag 360
 gttagagcag aagtaattcc tgaagcaaag gggttagctg ttactaaaca aaaagcggaa 420
 gaagctaaaa aagaagcaga agtagctaag agaaaatatg attatgcaac tctaaaggta 480
 gcactagcga agaaagaagt agaggctaag gaacttgaaa ttgaaaaact tcaatatgaa 540
 atttctactt tggaacaaga agttgctatt gctcaacatc aagtagataa tttgaaaaaa 600
 cttcttgctg gtgcggatcc tgatgatggc acaaaagtta tagaagctaa attaaacaaa 660
 ggagaagctg agctaaacgc taaacaagct gagttagcaa aaaaacaaac agaacttgaa 720
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 gctgaagctg agttggataa aaaagctgat gaacttcaaa ataaagttgc tgatttagaa 840
 aaaggaattg ctcttatca aatcaaagtc gctgaattaa ataaagaaat tgctagactt 900
 caaagcgatt taaaagatgc tgaagaaaat aatgtagaag actatattaa agaagggtta 960
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 cctgaaggta aaactcaaga tgaattagat aaagaagctg cagaagatgc taatattgaa 1140
 gctcttcaaa acaaagttgc tgatctagaa aacaaggttg ctgaattaga taaagaagtt 1200
 actagacttc aaagcgattt aaaagatgct gaagaaaaca atgtagaaga ctacgttaaa 1260
 gaaggcttag ataaagctct tactgataaa aaagttgaat taaataatac tcaaaaagca 1320
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<210> 18
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 <212> PRT

<220>
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Ala Lys Lys Lys Ala Glu Asp Ala Gln Lys Lys Tyr Asp Glu Asp Gln
 35 40 45
 Lys Lys Thr Glu Ala Lys Ala Asp Lys Glu Ala Lys Ala Ser Ala Glu
 50 55 60
 Ile Asp Lys Ala Thr Phe Ala Val Gln Ser Ala Tyr Val Lys Phe Leu
 65 70 75 80
 Asn Val Gln Ser Asn Arg Gln Ile Ser Glu Asn Glu Arg Lys Lys Gln
 85 90 95
 Leu Ala Glu Ile Asp Lys Glu Ile Glu Asn Ala Lys Gln Asn Leu Gln
 100 105 110
 Asn Lys Gln Glu Glu Phe Asn Lys Val Arg Ala Glu Val Ile Pro Glu
 115 120 125
 Ala Lys Gly Leu Ala Val Thr Lys Gln Lys Ala Glu Glu Ala Lys Lys
 130 135 140
 Glu Ala Glu Val Ala Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val
 145 150 155 160
 Ala Leu Ala Lys Lys Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys
 165 170 175
 Leu Gln Tyr Glu Ile Ser Thr Leu Glu Gln Glu Val Ala Ile Ala Gln
 180 185 190
 His Gln Val Asp Asn Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp
 195 200 205
 Asp Gly Thr Lys Val Ile Glu Ala Lys Leu Asn Lys Gly Glu Ala Glu
 210 215 220
 Leu Asn Ala Lys Gln Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu
 225 230 235 240
 Lys Leu Leu Asp Ser Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu
 245 250 255
 Asp Lys Glu Ala Ala Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu
 260 265 270
 Gln Asn Lys Val Ala Asp Leu Glu Lys Gly Ile Ala Pro Tyr Gln Ile
 275 280 285
 Lys Val Ala Glu Leu Asn Lys Glu Ile Ala Arg Leu Gln Ser Asp Leu
 290 295 300
 Lys Asp Ala Glu Glu Asn Asn Val Glu Asp Tyr Ile Lys Glu Gly Leu
 305 310 315 320
 Glu Gln Ala Ile Ala Asp Lys Lys Ala Glu Leu Ala Thr Thr Gln Gln
 325 330 335
 Asn Ile Asp Lys Thr Gln Lys Asp Leu Glu Asp Ala Glu Leu Glu Leu
 340 345 350
 Glu Lys Val Leu Ala Thr Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu
 355 360 365
 Leu Asp Lys Glu Ala Ala Glu Asp Ala Asn Ile Glu Ala Leu Gln Asn
 370 375 380
 Lys Val Ala Asp Leu Glu Asn Lys Val Ala Glu Leu Asp Lys Glu Val
 385 390 395 400
 Thr Arg Leu Gln Ser Asp Leu Lys Asp Ala Glu Glu Asn Asn Val Glu
 405 410 415
 Asp Tyr Val Lys Glu Gly Leu Asp Lys Ala Leu Thr Asp Lys Lys Val
 420 425 430
 Glu Leu Asn Asn Thr Gln Lys Ala Leu Asp Thr Ala Gln Lys Ala Leu
 435 440 445
 Asp Thr Ala Leu Asn Glu Leu Gly Pro Asp Gly
 450 455

<210> 19

<211> 34

<212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 19
 ctgaggatcc ttactaagct gtaaccttag tctc

34

<210> 20
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 <212> DNA
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<220>
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37

<210> 21
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 21
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37

<210> 22
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 <212> PRT
 <213> Streptococcus pneumoniae

<400> 22
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 1 5

<210> 23
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 <212> PRT
 <213> Streptococcus pneumoniae

<400> 23
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 1 5

<210> 24
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 <212> PRT
 <213> Streptococcus pneumoniae

<400> 24
 Tyr Pro Gln Val Glu Asp Lys Val Glu Asn Asp
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<210> 25
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<400> 25
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<210> 26
<211> 33
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